SEQUENCE LISTING

(1)   GENERAL INFORMATION:

    (i)   APPLICANT: Nelson, Edward L.
                              Nelson, Peter J.

    (ii)   TITLE OF INVENTION: NOVEL VECTOR FOR
                POLYNUCLEOTIDE VACCINES

    (iii)   NUMBER OF SEQUENCES: 29

    (iv)   CORRESPONDENCE ADDRESS:
                (A)   ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
                (B)   STREET: 345 PARK AVENUE
                (C)   CITY: NEW YORK
                (D)   STATE: NEW YORK
                (E)   COUNTRY: USA
                (F)   ZIP: 10154

    (v)   COMPUTER READABLE FORM:
                (A)   MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB
                (B)   COMPUTER: IBM PC COMPATIBLE
                (C)   OPERATING SYSTEM: PC-DOS/MS-DOS
                (D)   SOFTWARE: WORDPERFECT 5.1

    (vi)   CURRENT APPLICATION DATA:
                (A)   APPLICATION NUMBER: PCT/US97/14306
                (B)   FILING DATE: 14-AUG-1997

    (vii)   PRIOR APPLICATION DATA:
                (A)   APPLICATION NUMBER: US60/023931
                (B)   FILING DATE: 14-AUG-1996

    (viii) ATTORNEY/AGENT INFORMATION:
                (A)   NAME: KATHRYN M. BROWN
                (B)   REGISTRATION NUMBER: 34556
                (C)   REFERENCE/DOCKET NUMBER: 2026-4236US1

    (ix)   TELECOMMUNICATION INFORMATION:
                (A)   TELEPHONE: (212) 758-4800
                (B)   TELEFAX: (212) 751-6849
                (C)   TELEX: 421792

(2)   INFORMATION FOR SEQ ID NO:1:

    (i)   SEQUENCE CHARACTERISTICS:
                (A)   LENGTH: 453 base pairs
                (B)   TYPE: nucleic acid
                (C)   STRANDEDNESS: single
                (D)   TOPOLOGY: unknown

    (ii)   MOLECULE TYPE: cDNA

(iii)   HYPOTHETICAL: No

(iv)   ANTI-SENSE: No

(xi)   SEQUENCE DESCRIPTION:SEQ ID NO:1:

```
GGCCGCGTTG CTGGCGTTTT TCCATAGGCT CCGCCCCCCT      40
GACGAGCATC ACAAAAATCG ACGCTCAAGT CAGAGGTGGC      80
GAAACCCGAC AGGACTATAA AGATACCAGG CGTTTCCCCC     120
TGGAAGCTCC CTCGTGCGCT CTCCTGTTCC GACCCTGCCG     160
CTTACCGGAT ACCTCTCCGC CTTTCTCCCT TCGGGAAGCG     200
TGGCGCTTTC TCAATGCTCA CGCTGTAGGT ATCTCAGTTC     240
GGTGTAGGTC GTTCGCTCCA AGCTGGGCTG TGTGCACGAA     280
CCCCCCGTTC AGCCCGACCG CTGCGCCTTA TCCGGTAACT     320
ATCGTCTTGA GTCCAACCCG GTAAGACACG ACTTATCGCC     360
ACTGGCAGCA GCCACTGGTA ACAGGATTAG CAGAGCGAGG     400
TATGTAGGCG GTGCTACAGA GTTCTTGAAG TGGTGGCCTA     440
ACTACGGCTA CAC                                  453
```

(2)   INFORMATION FOR SEQ ID NO:2:

 (i)   SEQUENCE CHARACTERISTICS:
  (A)   LENGTH: 453 base pairs
  (B)   TYPE: nucleic acid

  (C)   STRANDEDNESS: single
  (D)   TOPOLOGY: unknown

 (ii)   MOLECULE TYPE: cDNA

 (iii)   HYPOTHETICAL: No

 (iv)   ANTI-SENSE: No

 (xi)   SEQUENCE DESCRIPTION:SEQ ID NO:2:

```
GTGTAGCCGT AGTTAGGCCA CCACTTCAAG AACTCTGTAG      40
CACCGCCTAC ATACCTCGCT CTGCTAATCC TGTTACCAGT      80
GGCTGCTGCC AGTGGCGATA AGTCGTGTCT TACCGGGTTG     120
GACTCAAGAC GATAGTTACC GGATAAGGCG CAGCGGTCGG     160
GCTGAACGGG GGGTTCGTGC ACACAGCCCA GCTTGGAGCG     200
AACGACCTAC ACCGAACTGA GATACCTACA CCGTGAGCAT     240
TGAGAAAGCG CCACGCTTCC CGAAGGGAGA AAGGCGGACA     280
GGTATCCGGT AAGCGGCAGG GTCGGAACAG GAGAGCGCAC     320
GAGGGAGCTT CCAGGGGGAA ACGCCTGGTA TCTTTATAGT     360
CCTGTCGGGT TTCGCCACCT CTGACTTGAG CGTCGATTTT     400
TGTGATGCTC GTCAGGGGGG CGGAGCCTAT GGAAAAACGC     440
CAGCAACGCG GCC                                  453
```

(2)   INFORMATION FOR SEQ ID NO:3:

 (i)   SEQUENCE CHARACTERISTICS:
  (A)   LENGTH: 209 base pairs

                    (B)   TYPE: nucleic acid
                    (C)   STRANDEDNESS: single
                    (D)   TOPOLOGY: unknown

          (ii)   MOLECULE TYPE: cDNA

          (iii)   HYPOTHETICAL: No

          (iv)   ANTI-SENSE: No

          (xi)   SEQUENCE DESCRIPTION:SEQ ID NO:3:

GAATTCTTTC GGACTTTTGA AAGTGATGGT GGTGGCCGAA   40
GGATTCGAAC CTTCGAAGTC GATGACGGCA GATTTAGAGT   80
CTGCTCCCTT TGGCCGCTCG GGAACCCCAC CACGGGTAAT   120
GCTTTTACTG GCCTGCTCCC TTATCGGGAA GCGGGGCGCA   160
TCATATCAAA TGACGCGCCG CTGTAAAGTG TTACGTTGAG   200
AAAGAATTC   209

(2)   INFORMATION FOR SEQ ID NO:4:

          (i)   SEQUENCE CHARACTERISTICS:
                    (A)   LENGTH: 209 base pairs

                    (B)   TYPE: nucleic acid
                    (C)   STRANDEDNESS: single
                    (D)   TOPOLOGY: unknown

          (ii)   MOLECULE TYPE: cDNA

          (iii)   HYPOTHETICAL: No

          (iv)   ANTI-SENSE: No

          (xi)   SEQUENCE DESCRIPTION:SEQ ID NO:4:

GAATTCTTTC TCAACGTAAC ACTTTACAGC GGCGCGTCAT   40
TTGATATGAT GCGCCCCGCT TCCCGATAAG GGAGCAGGCC   80
AGTAAAAGCA TTACCCGTGG TGGGGTTCCC GAGCGGCCAA   120
AGGGAGCAGA CTCTAAATCT GCCGTCATCG ACTTCGAAGG   160
TTCGAATCCT TCCCCCACCA CCATCACTTT CAAAAGTCCG   200
AAAGAATTC   209

(2)   INFORMATION FOR SEQ ID NO:5:

          (i)   SEQUENCE CHARACTERISTICS:
                    (A)   LENGTH: 6 base pairs
                    (B)   TYPE: nucleic acid
                    (C)   STRANDEDNESS: single
                    (D)   TOPOLOGY: unknown

          (ii)   MOLECULE TYPE: cDNA

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(iii)   HYPOTHETICAL: No

(xi)   SEQUENCE DESCRIPTION:SEQ ID NO:5:

AATAAA   6

(2)   INFORMATION FOR SEQ ID NO:6:

    (i)   SEQUENCE CHARACTERISTICS:
          (A)   LENGTH: 6 base pairs
          (B)   TYPE: nucleic acid
          (C)   STRANDEDNESS: single
          (D)   TOPOLOGY: unknown

    (ii)   MOLECULE TYPE: cDNA

    (iii)   HYPOTHETICAL: No

    (iv)   ANTI-SENSE: No

    (xi)   SEQUENCE DESCRIPTION:SEQ ID NO:6:

ATTAAA   6

(2)   INFORMATION FOR SEQ ID NO:7:

    (i)   SEQUENCE CHARACTERISTICS:
          (A)   LENGTH: 6 base pairs
          (B)   TYPE: nucleic acid
          (C)   STRANDEDNESS: single
          (D)   TOPOLOGY: unknown

    (ii)   MOLECULE TYPE: cDNA

    (iii)   HYPOTHETICAL: No

    (xi)   SEQUENCE DESCRIPTION:SEQ ID NO:7:

AGTAAA   6

(2)   INFORMATION FOR SEQ ID NO:8:

    (i)   SEQUENCE CHARACTERISTICS:
          (A)   LENGTH: 6 base pairs
          (B)   TYPE: nucleic acid
          (C)   STRANDEDNESS: single
          (D)   TOPOLOGY: unknown

    (ii)   MOLECULE TYPE: cDNA

(iii)   HYPOTHETICAL: No

(xi)   SEQUENCE DESCRIPTION:SEQ ID NO:8:

AAGAAC   6

(2)   INFORMATION FOR SEQ ID NO:9:

        (i)   SEQUENCE CHARACTERISTICS:
                    (A)   LENGTH: 6 base pairs
                    (B)   TYPE: nucleic acid
                    (C)   STRANDEDNESS: single
                    (D)   TOPOLOGY: unknown

        (ii)   MOLECULE TYPE: cDNA

        (iii)   HYPOTHETICAL: No

        (iv)   ANTI-SENSE: No

        (xi)   SEQUENCE DESCRIPTION:SEQ ID NO:9:

AATACA   6

(2)   INFORMATION FOR SEQ ID NO:10:

        (i)   SEQUENCE CHARACTERISTICS:
                    (A)   LENGTH: 227 base pairs
                    (B)   TYPE: nucleic acid
                    (C)   STRANDEDNESS: single
                    (D)   TOPOLOGY: unknown

        (ii)   MOLECULE TYPE: cDNA

        (iii)   HYPOTHETICAL: No

        (iv)   ANTI-SENSE: No

        (xi)   SEQUENCE DESCRIPTION:SEQ ID NO:10:

GCCTTAAGGG CCATATGGTG AGTGGATCCC TTGACCCCAG   40
GCGGGGATGG GGAGACCTGT AGTCAGAGCC CCCGGGCAGC   80
ACAGGCCAAT GCCCGTCCTT CCCCTGCAGG ATGAGTAGTG   120
AGTGCCTCTC CTGGCCCTGG AAGTTGCCAC TCCAGTGCCC   160
ACCAGCCTTG TCCTAATAAA ATTAAGTTGC ATCATTTTGT   200
CTGACTAGGT GTCCTCTATA ATATTAT   227

(2)   INFORMATION FOR SEQ ID NO:11:

        (i)   SEQUENCE CHARACTERISTICS:
                    (A)   LENGTH: 227 base pairs
                    (B)   TYPE: nucleic acid

```
            (C)    STRANDEDNESS:  single
            (D)    TOPOLOGY:  unknown

    (ii)    MOLECULE TYPE:  cDNA

    (iii)   HYPOTHETICAL:  No

    (iv)    ANTI-SENSE:  No

    (xi)    SEQUENCE DESCRIPTION:SEQ ID NO:11:


ATAATATTAT AGAGGACACC TAGTCAGAAC AAATGATGCA            40
ACTTAATTTT ATTAGGACAA GGCTGGTGGG CACTGGAGTG            80
GCAACTTCCA GGGCCAGGAG AGGCACTCAC TACTCATCCT           120
GCAGGGGAAG GACGGGCATT GGCCTGTGCT GCCCGGGGGC           160
TCTGACTACA GGTCTCCCCC ATCCCCGCCT GGGGTCAAGG           200
CATCCACTCA CCATATGGCC CTTAAGG                         227


(2)    INFORMATION FOR SEQ ID NO:12:

            (i)    SEQUENCE CHARACTERISTICS:
                   (A)    LENGTH:  252 base pairs
                   (B)    TYPE:  nucleic acid
                   (C)    STRANDEDNESS:  single
                   (D)    TOPOLOGY:  unknown

            (ii)    MOLECULE TYPE:  cDNA

            (iii)   HYPOTHETICAL:  No

            (iv)    ANTI-SENSE:  No

            (xi)    SEQUENCE DESCRIPTION:SEQ ID NO:12:


CCTCGGTACC TGCCATGGCG CGGATTCTTT ATCACTGATA            40
AGTTGGTGGA CATATTATGT TTATCAGTGA TAAAGTGTCA            80
AGCATGACAA AGTTGCAGCC GAATACAGTG ATCCGTGCCG           120
GCCCTGGACT GTTGAACGAG GTCGGCGTAG ACGGTCTGAC           160
GACACGCAAA CTGGCGGAAC GGTTGGGGGT GCAGCAGCCG           200
GCGCTTTACT GGCACTTCAG GAACAAGCGG GCGCCTTAAG           240
GGCCATATGC CG                                         252


(2)    INFORMATION FOR SEQ ID NO:13:

            (i)    SEQUENCE CHARACTERISTICS:
                   (A)    LENGTH:  35 base pairs
                   (B)    TYPE:  nucleic acid


                   (C)    STRANDEDNESS:  single
                   (D)    TOPOLOGY:  unknown
```

(ii)   MOLECULE TYPE: cDNA

(iii)   HYPOTHETICAL: No

(iv)   ANTI-SENSE: No

(xi) SEQUENCE DESCRIPTION:SEQ ID NO:13:

CCTCGGTACC TGCCACCATG GCGCGGATTC TTTAT   35

(2)   INFORMATION FOR SEQ ID NO:14:

      (i)   SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 38 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: unknown

      (ii)   MOLECULE TYPE: cDNA

      (iii) HYPOTHETICAL: No

      (iv)   ANTI-SENSE: No

      (xi) SEQUENCE DESCRIPTION:SEQ ID NO:14:

CGGCATATGG CCTTAAGGCG CCCGCTTGTT CCTGAAGT   38

(2)   INFORMATION FOR SEQ ID NO:15:

      (i)   SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 228 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: unknown

      (ii)   MOLECULE TYPE: cDNA

      (iii) HYPOTHETICAL: No

      (iv)   ANTI-SENSE: No

      (xi) SEQUENCE DESCRIPTION:SEQ ID NO:15:

```
GCCTTAAGGG CCATATGGTG AGTGGATGCC TTGACCCCAG        40
GCGGGGATGG GGGAGACCTG TAGTCAGAGC CCCCGGGCAG        80

CACAGGCCAA TGCCCGTCCT TCCCCTGCAG GATGAGTAGT        120
GAGTGCCTCT CCTGGCCCTG GAAGTTGCCA CTCCAGTGCC        160
CACCAGCCTT GTCCTAATAA AATTAAGTTG CATCATTTTG        200
TCTGACTAGG TGTCCTCTAT AATATTAT                     228
```

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(2)   INFORMATION FOR SEQ ID NO:16:

    (i)   SEQUENCE CHARACTERISTICS:
        (A)   LENGTH: 1425 base pairs
        (B)   TYPE: nucleic acid
        (C)   STRANDEDNESS: single
        (D)   TOPOLOGY: unknown

    (ii)   MOLECULE TYPE: cDNA

    (iii)   HYPOTHETICAL: No

    (iv)   ANTI-SENSE: No

    (xi)   SEQUENCE DESCRIPTION:SEQ ID NO:16:

```
TGCCATGGCG CGGATTCTTT ATCACTGATA AGTTGGTGGA        40
CATATTATGT TTATCAGTGA TAAAGTGTCA AGCATGACAA        80
AGTTGCAGCC GAATACAGTG ATCCGTGCCG GCCCTGGACT       120
GTTGAACGAG GTCGGCGTAG ACGGTCTGAC GACACGCAAA       160
CTGGCGGAAC GGTTGGGGGT GCAGCAGCCG GCGCTTTACT       200
GGCACTTCAG GAACAAGCGG GCGCCTTAAG GGCCATATGG       240
TGAGTGGATG CCTTGACCCC AGGCGGGGAT GGGGGAGACC       280
TGTAGTCAGA GCCCCCGGGC AGCACAGGCC AATGCCCGTC       320
CTTCCCCTGC AGTGAGTAGT GACTGCCCGG GTGGGATCCC       360
TGTGACCCCT CCCCAGTGCC TCTCCTGGCC CTGGAAGTTG       400
CCACTCCAGT GCCCACCAGC CTTGTCCTAA TAAAATTAAG       440
TTGCATCATT TTGTCTGACT AGGTGTCCTC TATAATATTA       480
TAAGCTTGAT ATCGAATTCT TTCTCAACGT AACACTTTAC       520
AGCGGCGCGT CATTTGATAT GATGCGCCCC GCTTCCCGAT       560
AAGGGAGCAG GCCAGTAAAA GCATTACCCG TGGTGGGGTT       600
CCCGAGCGGC CAAAGGGAGC AGACTCTAAA TCTGCCGTCA       640
TCGACTTCGA AGGTTCGAAT CCTTCCCCCA CCACCATCAC       680
TTTCAAAAGT CCGAAAGAAT TCCTGCAGCC CGTGTAGCCG       720
TAGTTAGGCC ACCACTTCAA GAACTCTGTA GCACCGCCTA       760
CATACCTCGC TCTGCTAATC CTGTTACCAG TGGCTGCTGC       800
CAGTGGCGAT AAGTCGTGTC TTACCGGGTT GGACTCAAGA       840
CGATAGTTAC CGGATAAGGC GCAGCGGTCG GGCTGAACGG       880
GGGGTTCGTG CACACAGCCC AGCTTGGAGC GAACGACCTA       920
CACCGAACTG AGATACCTAC AGCGTGAGCA TTGAGAAAGC       960
GCCACGCTTC CCGAAGGGAG AAAGGCGGAC AGGTATCCGG      1000
TAAGCGGCAG GGTCGGAACA GGAGAGCGCA CGAGGGAGCT      1040
TCCAGGGGGA AACGCCTGGT ATCTTTATAG TCCTGTCGGG      1080
TTTCGCCACC TCTGACTTGA GCGTCGATTT TTGTGATGCT      1120
CGTCAGGGGG GCGGAGCCTA TGGAAAAACG CCAGCAACGC      1160
GGCCGGGGGA TCCGGAGAGC TCACTCTAGA TGAGAGAGCA      1200
GTGAGGGAGA GACAGAGACT CGAATTCCG GAGCTATTTC       1240
AGTTTTCTTT TCCGTTTTGT GCAATTTCAC TTATGATACC      1280

GGCCAATGCT TGGTTGCTAT TTTGGAAACT CCCCTTAGGG      1320
GATGCCCCTC AACTGGCCCT ATAAAGGGCC AGCCTGAGCT      1360
GCAGAGGATT CCTGCAGAGG ATCAAGACAG CACGTGGACC      1400
TCGCACAGCC TCTCCCACAG GTACC                      1425
```

(2)   INFORMATION FOR SEQ ID NO:17:

    (i)   SEQUENCE CHARACTERISTICS:
       (A)   LENGTH: 719 base pairs
       (B)   TYPE: nucleic acid
       (C)   STRANDEDNESS: single
       (D)   TOPOLOGY: unknown

    (ii)   MOLECULE TYPE: cDNA

    (iii)   HYPOTHETICAL: No

    (iv)   ANTI-SENSE: No

    (xi)   SEQUENCE DESCRIPTION:SEQ ID NO:17:

```
ATGAGCAAGG GCGAGGAACT GTTCACTGGC GTGGTCCCAA          40
TTCTCGTGGA ACTGGATGGC GATGTGAATG GGCACAAATT          80
TTCTGTCAGC GGAGAGGGTG AAGGTGATGC CACATACGGA         120
AAGCTCACCC TGAAATTCAT CTGCACCACT GGAAAGCTCC         160
CTGTGCCATG GCCAACACTG GTCACTACCT TCACCTATGG         200
CGTGCAGTGC TTTTCCAGAT ACCCAGACCA TATGAACGAG         240
CATGACTTTT TCAAGAGCGC CATGCCCGAG GGCTATGTGC         280
AGGAGAGAAC CATCTTTTTC AAAGATGACG GGAACTACAA         320
GACCCGCGCT GAAGTCAAGT TCGAAGGTGA CACCCTGGTG         360
AATAGAATCG AGTTGAAGGG CATTGACTTT AAGGAAGATG         400
GAAACATTCT CGGCCACAAG CTGGAATACA ACTATAACTC         440
CCACAATGTG TACATCATGG CCGACAAGCA AAAGAATGGC         480
ATCAAGGTCA ACTTCAAGAT CAGACACAAC ATTGAGGATG         520
GATCCGTGCA GCTGGCCGAC CATTATCAAC AGAACACTCC         560
AATCGGCGAC CGCCCTGTGC TCCTCCCAGA CAACAATTAC         600
CTGTCCACCC AGTCTGCCCT GTCTAAAGAT CCCAACGAAA         640
AGAGAGACCA CATGGTCCTG CTGGAGTTTG TGACCGCTGC         680
TGGGATCACA CATGGCATGG ACGAGCTGTA CAAGTGAGC          719
```

(2)   INFORMATION FOR SEQ ID NO:18:

    (i)   SEQUENCE CHARACTERISTICS:
       (A)   LENGTH: 1911 base pairs
       (B)   TYPE: nucleic acid
       (C)   STRANDEDNESS: single
       (D)   TOPOLOGY: unknown

    (ii)   MOLECULE TYPE: cDNA

    (iii)   HYPOTHETICAL: No

    (iv)   ANTI-SENSE: No

    (xi)   SEQUENCE DESCRIPTION:SEQ ID NO:18:

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```
TATGAGCAAG GGCGAGGAAC TGTTCACTGG CGTGGTCCCA        40
ATTCTCGTGG AACTGGATGG CGATGTGAAT GGGCACAAAT        80
TTTCTGTCAG CGGAGAGGGT GAAGGTGATG CCACATACGG       120
AAAGCTCACC CTGAAATTCA TCTGCACCAC TGGAAAGCTC       160
CCTGTGCCAT GGCCAACACT GGTCACTACC TTCACCTATG       200
GCGTGCAGTG CTTTTCCAGA TACCCAGACC ATATGAAGCA       240
GCATGACTTT TTCAAGAGCG CCATGCCCGA GGGCTATGTG       280
CAGGAGAGAA CCATCTTTTT CAAAGATGAC GGGAACTACA       320
AGACCCGCGC TGAAGTCAAG TTCGAAGGTG ACACCCTGGT       360
GAATAGAATC GAGTTGAAGG GCATTGACTT TAAGGAAGAT       400
GGAAACATTC TCGGCCACAA GCTGGAATAC AACTATAACT       440
CCCACAATGT GTACATCATG GCCGACAAGC AAAAGAATGG       480
CATCAAGGTC AACTTCAAGA TCAGACACAA CATTGAGGAT       520
GGATCCGTGC AGCTGGCCGA CCATTATCAA CAGAACACTC       560
CAATCGGCGA CGGCCCTGTG CTCCTCCCAG ACAACCATTA       600
CCTGTCCACC CAGTCTGCCC GTCTAAAGAT CCCAACGAAA       640
AGAGAGACCA CATGGTCCTG CTGGAGTTTG TGACCGCTGC       680
TGGGATCACA CATGGCATGG ACGAGCTGTA CAAGTGAGCC       720
ATATGGTGAG TGGATGCCTT GACCCCAGGC GGGGATGGGG       760
GAGACCTGTA GTCAGAGCCC CCGGGCAGCA CAGGCCAATG       800
CCCGTCCTTC CCCTGCAGTG AGTAGTGACT GCCCGGGTGG       840
GATCCCTGTG ACCCCTCCCC AGTGCCTCTC CTGGCCCTGG       880
AAGTTGCCAC TCCAGTGCCC ACCAGCCTTG TCCTAATAAA       920
ATTAAGTTGC ATCATTTTGT CTGACTAGGT GTCCTCTATA       960
ATATTATAAG CTTGATATCG AATTCTTTCT CAACGTAACA      1000
CTTTACAGCG GCGCGTCATT TGATATGATG CGCCCCGCTT      1040
CCCGATAAGG GAGCAGGCCA GTAAAAGCAT TACCCGTGGT      1080
GGGGTTCCCG AGCGGCCAAA GGGAGCAGAC TCTAAATCTG      1120
CCGTCATCGA CTTCGAAGGT TCGAATCCTT CCCCCACCAC      1160
CATCACTTTC AAAAGTCCGA AAGAATTCCT GCAGCCCGTG      1200
TAGCCGTAGT TAGGCCACCA CTTCAAGAAC TCTGTAGCAC      1240
CGCCTACATA CCTCGCTCTG CTAATCCTGT TACCAGTGGC      1280
TGCTGCCAGT GGCGATAAGT CGTGTCTTAC CGGGTTGGAC      1320
TCAAGACGAT AGTTACCGGA TAAGGCGCAG CGGTCGGGCT      1360
GAACGGGGGG TTCGTGCACA CAGCCCAGCT TGGAGCGAAC      1400
GACCTACACC GAACTGAGAT ACCTACAGCG TGAGCATTGA      1440
GAAAGCGCCA CGCTTCCCGA AGGGAGAAAG GCGGACAGGT      1480
ATCCGGTAAG CGGCAGGGTC GGAACAGGAG AGCGCACGAG      1520
GGAGCTTCCA GGGGGAAACG CCTGGTATCT TTATAGTCCT      1560
GTCGGGTTTC GCCACCTCTG ACTTGAGCGT CGATTTTTGT      1600
GATGCTCGTC AGGGGGGCGG AGCCTATGGA AAAACGCCAG      1640
CAACGCGGCC GGGGGATCCG GAGAGCTCAC TCTAGATGAG      1680
AGAGCAGTGA GGGAGAGACA GAGACTCGAA TTTCCGGAGC      1720
TATTTCAGTT TTCTTTTCCG TTTTGTGCAA TTTCACTTAT      1760
GATACCGGCC AATGCTTGGT TGCTATTTTG GAAACTCCCC      1800
TTAGGGGATG CCCCTCAACT GGCCCTATAA AGGGCCAGCC      1840
TGAGCTGCAG AGGATTCCTG CAGAGGATCA AGACAGCACG      1880
TGGACCTCGC ACAGCCTCTC CCACAGGTAC C                1911
```

(2)   INFORMATION FOR SEQ ID NO:19:

      (i)   SEQUENCE CHARACTERISTICS:
            (A)   LENGTH: 69 amino acids
            (B)   TYPE: amino acid
            (D)   TOPOLOGY: unknown

(ii)   MOLECULE TYPE: peptide

(xi)   SEQUENCE DESCRIPTION:SEQ ID NO:19:

Pro Asp Leu Ser Tyr Met Pro Ile Trp Lys Phe Pro
 1   5   10
Asp Glu Glu Gly Ala Cys Gln Pro Cys Pro Ile Asn
             15   20
Cys Thr His Ser Cys Val Asp Leu Asp Asp Lys Gly
25   30   35
Cys Pro Ala Glu Gln Arg Ala Ser Pro Leu Thr Ser
             40   45
Ile Ile Ser Ala Val Val Gly Ile Leu Leu Val Val
             50   55   60
Val Leu Gly Val Val Phe Gly Ile Leu
             65

(2)   INFORMATION FOR SEQ ID NO:20:

        (i)   SEQUENCE CHARACTERISTICS:
                (A)   LENGTH: 287 amino acids
                (B)   TYPE: amino acid
                (D)   TOPOLOGY: unknown

        (ii)   MOLECULE TYPE: protein

        (xi)   SEQUENCE DESCRIPTION:SEQ ID NO:20:

Pro Ala Pro Gly Ala Gly Gly Met Val His His Arg
 1   5   10
His Arg Ser Ser Ser Thr Arg Ser Gly Gly Gly Asp
             15   20
Leu Thr Leu Gly Leu Glu Pro Ser Glu Glu Glu Ala
25   30   35
Pro Arg Ser Pro Leu Ala Pro Ser Glu Gly Ala Gly
             40   45
Ser Asp Val Phe Asp Gly Asp Leu Gly Met Gly Ala
             50   55   60
Ala Lys Gly Leu Ser Leu Pro Thr His Asp Pro Ser
             65   70
Pro Leu Gln Arg Tyr Ser Glu Asp Pro Thr Val Pro
             75   80
Leu Pro Ser Glu Thr Asp Gly Tyr Val Ala Pro Leu
85   90   95

Thr Cys Ser Pro Gln Pro Glu Tyr Val Asn Gln Pro
             100   105
Asp Val Arg Pro Pro Pro Ser Pro Arg Glu Gly Pro
             110   115   120

Leu Pro Ala Ala Arg Pro Ala Gly Ala Thr Leu Glu
                 125   130
Arg Pro Lys Thr Leu Ser Pro Gly Lys Asn Gly Val
             135   140

```
Val Lys Asp Val Phe Ala Phe Gly Gly Ala Val Glu
145             150             155
Asn Pro Glu Tyr Leu Thr Pro Gln Gly Thr Cys Ser
            160             165
Pro Gln Pro Glu Tyr Val Asn Gln Pro Asp Val Arg
        170             175             180
Pro Gln Pro Pro Ser Pro Arg Glu Gly Pro Leu Pro
                185             190
Ala Ala Arg Pro Ala Gly Ala Thr Leu Glu Arg Pro
            195             200
Lys Leu Ser Pro Gly Lys Asn Gly Val Val Lys Asp
205             210             215
Val Phe Ala Phe Gly Gly Ala Val Glu Asn Pro Glu
        220             225
Tyr Leu Thr Pro Gln Gly Gly Ala Ala Pro Gln Pro
    230             235             240
His Pro Pro Pro Ala Phe Ser Pro Ala Phe Asp Asn
                245             250
Leu Tyr Tyr Trp Asp Asp Pro Pro Glu Arg Gly Ala
        255             260
Pro Pro Ser Thr Phe Lys Gly Thr Pro Thr Ala Glu
260             270             275
Asn Pro Glu Tyr Leu Gly Leu Asp Val Pro Val
            280             285
```

(2)   INFORMATION FOR SEQ ID NO:21:

      (i)   SEQUENCE CHARACTERISTICS:
            (A)   LENGTH: 22 amino acids
            (B)   TYPE: amino acid
            (D)   TOPOLOGY: unknown

      (ii)   MOLECULE TYPE: peptide

      (xi) SEQUENCE DESCRIPTION:SEQ ID NO:21:

```
Ile Ile Ser Ala Val Val Gly Ile Leu Leu Val Val
 1               5                   10

Val Leu Gly Val Val Phe Gly Ile Leu Ile
            15              20
```

(2)   INFORMATION FOR SEQ ID NO:22:

      (i)   SEQUENCE CHARACTERISTICS:
            (A)   LENGTH: 2125 base pairs
            (B)   TYPE: nucleic acid
            (C)   STRANDEDNESS: single

            (D)   TOPOLOGY: unknown

(ii)   MOLECULE TYPE: cDNA

(iii)   HYPOTHETICAL: No

(iv)   ANTI-SENSE: No

(xi)   SEQUENCE DESCRIPTION:SEQ ID NO:22:

```
GCCACCATGG CCCCTGACCT CTCCTACATG CCCATCTGGA          40
AGTTTCCAGA TGAGGAGGGC GCATGCCAGC CTTGCCCCAT          80
CAACTGCACC CACTCCTGTG TGGACCTGGA TGACAAGGGC         120
TGCCCCGCCG AGCAGAGAGC CAGCCCTCTG ACGTCCATCA         160
TCTCTGCGGT GGTTGGCATT CTGCTGGTCG TGGTCTTGGG         200
GGTGGTCTTT GGGATCCTCA TCAAGCGACG GCAGCAGAAG         240
ATCACATGTC CAGACCCTGC CCCGGGCGCT GGGGGCATGG         280
TCCACCACAG GCACCGCAGC TCATCTACCA GGAGTGGCGG         320
TGGGGACCTG ACACTAGGGC TGGAGCCCTC TGAAGAGGAG         360
GCCCCCAGGT CTCCACTGGC ACCCTCCGAA GGGGCTGGCT         400
CCGATGTATT TGATGGTGAC CTGGGAATGG GGGCAGCCAA         440
GGGGCTGCAA AGCCTCCCCA CACATGACCC CAGCCCTCTA         480
CAGCGGTACA GTGAGGACCC CACAGTACCC CTGCCCTCTG         520
AGACTGATGG CTACGTTGCC CCCCTGACCT GCAGCCCCCA         560
GCCTGAATAT GTGAACCAGC CAGATGTTCG GCCCCAGCCC         600
CCTTCGCCCC GAGAGGGCCC TCTGCCTGCT GCCCGACCTG         640
CTGGTGCCAC TCTGGAAAGG CCCAAGACTC TCTCCCCAGG         680
GAAGAATGGG GTCGTCAAAG ACGTTTTTGC CTTTGGGGGT         720
GCCGTGGAGA ACCCCGAGAC TTGACACCCC AGGGAGGAGC         760
TGCCCCTCAG CCCCACCCTC CTCCTGCCTT CAGCCCAGCC         800
TTCGACAACC TCTATTACTG GGACCAGGAC CCACCAGAGC         840
GGGGGGGCTCC ACCCAGCACC TTCAAAGGGA CACCTACGGC        880
AGAGAACCCA GAGTACCTGG GTCTGGACGT GCCAGTGTGA         920
AGCCTTAAGG GCCATATGGT GAGTGGATGC CTTGACCCCA         960
GGCGGGGATG GGGGAGACCT GTAGTCAGAG CCCCCGGGCA        1000
GCACAGGCCA ATGCCCGTCC TTCCCCTGCA GTGAGTAGTG        1040
ACTGCCCGGG TGGGATCCCT GTGACCCCTC CCCAGTGCCT        1080
CTCCTGGCCC TGGAAGTTGC CACTCCAGTG CCCACCAGCC        1120
TTGTCCTAAT AAAATTAAGT TGCATCATTT TGTCTGACTA        1160
GGTGTCCTCT ATAATATTAT AAGCTTGATA TCGAATTCTT        1200
TCTCAACGTA ACACTTTACA GCGGCGCGTC ATTTGATATG        1240
ATGCGCCCCG CTTCCCGATA AGGGAGCAGG CCAGTAAAAG        1280
CATTACCCGT GGTGGGGTTC CCGAGCGGCC AAAGGGAGCA        1320
GACTCTAAAT CTGCCGTCAT CGACTTCGAA GGTTCGAATC        1360
CTTCCCCCAC CACCATCACT TTCAAAGTC CGAAAGAATT         1400
CCTGCAGCCC GTGTAGCCGT AGTTAGGCCA CCACTTCAAG        1440
AACTCTGTAG CACCGCCTAC ATACCTCGCT CTGCTAATCC        1480
TGTTACCAGT GGCTGCTGCC AGTGGCGATA AGTCGTGTCT        1520
TACCGGGTTG GACTCAAGAC GATAGTTACC GGATAAGGCG        1560
CAGCGGTCGG GCTGAACGGG GGGTTCGTGC ACACAGCCCA        1600
GCTTGGAGCG AACGACCTAC ACCGAACTGA GATACCTACA        1640
GCGTGAGCAT TGAGAAAGCG CCACGCTTCC CGAAGGGAGA        1680
AAGGCGGACA GGTATCCGGT AAGCGGCAGG GTCGGAACAG        1720
GAGAGCGCAC GAGGGAGCTT CCAGGGGGAA ACGCCTGGTA        1760
TCTTTATAGT CCTGTCGGGT TTCGCCACCT CTGACTTGAG        1800
CGTCGATTTT TGTGATGCTC GTCAGGGGGG CGGAGCCTAT        1840
GGAAAAACGC CAGCAACGCG GCCGGGGGAT CCGGAGAGCT        1880
CACTCTAGAT GAGAGAGCAG TGAGGGAGAG ACAGAGACTC        1920
GAATTTCCGG AGCTATTTCA GTTTTCTTTT CCGTTTTGTG        1960
```

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```
CAATTTCACT TATGATACCG GCCAATGCTT GGTTGCTATT          2000
TTGGAAACTC CCCTTAGGGG ATGCCCCTCA ACTGGCCCTA          2040
TAAAGGGCCA GCCTGAGCTG CAGAGGATTC CTGCAGAGGA          2080
TCAAGACAGC ACGTGGACCT CGCACAGCCT CTCCCACAGG          2120
TACCT                                                2125
```

(2)   INFORMATION FOR SEQ ID NO:23:

    (i)   SEQUENCE CHARACTERISTICS:
           (A)   LENGTH: 27 base pairs
           (B)   TYPE: nucleic acid
           (C)   STRANDEDNESS: single
           (D)   TOPOLOGY: unknown

    (ii)   MOLECULE TYPE: oligonucleotide

    (iii)   HYPOTHETICAL: No

    (iv)   ANTI-SENSE: No

    (xi)   SEQUENCE DESCRIPTION:SEQ ID NO:23:

```
GTCTGCCACC ATGGCCTACT CCCCTGC                         27
```

(2)   INFORMATION FOR SEQ ID NO:24:

    (i)   SEQUENCE CHARACTERISTICS:
           (A)   LENGTH: 36 base pairs
           (B)   TYPE: nucleic acid
           (C)   STRANDEDNESS: single
           (D)   TOPOLOGY: linear

    (ii)   MOLECULE TYPE: oligonucleotide

    (iii)   HYPOTHETICAL: No

    (iv)   ANTI-SENSE: No

    (xi)   SEQUENCE DESCRIPTION:SEQ ID NO:24:

```
TTCTTTGGTG ACCTACCTCT TCGGAATTGC CGAGTC               36
```

(2)   INFORMATION FOR SEQ ID NO:25:

    (i)   SEQUENCE CHARACTERISTICS:
           (A)   LENGTH: 1242 base pairs
           (B)   TYPE: nucleic acid
           (C)   STRANDEDNESS: single
           (D)   TOPOLOGY: unknown

(ii)   MOLECULE TYPE: cDNA

(iii)   HYPOTHETICAL: No

(iv)   ANTI-SENSE: No

(xi)   SEQUENCE DESCRIPTION:SEQ ID NO:25:

```
ATGGAGGAGC CGCAGTCAGA TCCTAGCGTC GAGCCCCCTC        40
TGAGTCAGGA AACATTTTCA GACCTATGGA AACTACTTCC        80
TGAAAACAAC GTTCTGTCCC CCTTGCCGTC CCAAGCAATG       120
GATGATTTGA TGCTGTCCCC GGACGATATT GAACAATGGT       160
TCACTGAAGA CCCAGGTCCA GATGAAGCTC CCAGAATGCC       200
AGAGGCTGCT CCCCGCGTGG CCCCTGCACC AGCAGCTCCT       240
ACACCGGCGG CCCCTGCACC AGCCCCCTCC TGGCCCCTGT       280
CATCTTCTGT CCCTTCCCAG AAAACCTACC AGGGCAGCTA       320
CGGTTTCCGT CTGGGCTTCT TGCATTCTGG GACAGCCAAG       360
TCTGCCACCA TGGCCTACTC CCCTGCGTCT GTGACTTGCA       400
CGTACTCCCC TGCCCTCAAC AAGATGTTTT GCCAACTGGC       440
CAAGACCTGC CCTGTGCAGC TGTGGGTTGA TTCCACACCC       480
CCGCCCGGCA CCCGCGTCCG CGCCATGGCC ATCTACAAGC       520
AGTCACAGCA CATGACGGAG GTTGTGAGGC GCTGCCCCCA       560
CCATGAGCGC TGCTCAGATA GCGATGGTCT GGCCCCTCCT       600
CAGCGTCTTA TCCGAGTGGA AGGAAATTTG CGTGTGGAGT       640
ATTTGGATGA CAGAAACACT TTTCGACATA GTGTGGTGGT       680
GCCCTATGAG CCGCCTGAGG TTGGCTCTGA CTGTACCACC       720
ATCCACTACA ACTACATGTG TAACAGTTCC TGCATGGGCG       760
GCATGAACCG GAGGCCCATC CTCACCATCA TCACACTGGA       800
AGACTCCAGT GGTAATCTAC TGGGACGGAA CAGCTTTGAG       840
GTGCGTGTTT GTGCCTGTCC TGGGAGAGAC CGGCGCACAG       880
AGGAAGAGAA TCTCCGCAAG AAAGGGGAGC TCACCACGA       920
GCTGCCCCCA GGGAGCACTA AGCGAGCACT GCCCAACAAC       960
ACCAGCTCCT CTCCCCAGCC AAAGAAGAAA CCACTGGATG      1000
GAGAATATTT CACCCTTCAG ATCCGTGGGC GTGAGCGCTT      1040
CGAGATGTTC TTTGGTGACC TACCTCTTCG GAATTGCCGA      1080
GTCTTCCGAG AGCTGAATGA GGCCTTGGAA CTCAAGGATG      1120
CCCAGGCTGG GAAGGAGCCA GGGGGGAGCA GGGCTCACTC      1160
CAGCCACCTG AAGTCCAAAA AGGGTCAGTC TACCTCCCGC      1200
CATAAAAAAC TCATGTTCAA GACAGAAGGG CCTGACTCAG      1240
AC                                              1242
```

(2)   INFORMATION FOR SEQ ID NO:26:

    (i)   SEQUENCE CHARACTERISTICS:
        (A)   LENGTH: 608 base pairs
        (B)   TYPE: nucleic acid
        (C)   STRANDEDNESS: single
        (D)   TOPOLOGY: unknown

    (ii)   MOLECULE TYPE: cDNA

    (iii)   HYPOTHETICAL: No

(iv)   ANTI-SENSE: No

(xi)   SEQUENCE DESCRIPTION:SEQ ID NO:26:

```
CTCGGGCCGC  GTTGCTGGCG  TTTTTCCATA  GGCTCCGCCC      40
CCCTGACGAG  CATCACAAAA  ATCGACGCTC  AAGTCAGAGG      80
TGGCGAAACC  CGACAGGACT  ATAAAGATAC  CAGGCGTTTC     120
CCCCTGGAAG  CTCCCTCGTG  CGCTCTCCTG  TTCCGACCCT     160
GCCGCTTACC  GGATACCTGT  CCGCCTTTCT  CCCTTCGGGA     200
AGCGTGGCGC  TTTCTCAATG  CTCACGCTGT  AGGTATCTCA     240
GTTCGGTGTA  GGTCGTTCGC  TCCAAGCTGG  GCTGTGTGCA     280
CGAACCCCCC  GTTCAGCCCG  ACCGCTGCGC  CTTATCCGGT     320
AACTATCGTC  TTGAGTCCAA  CCCGGTAAGA  CACGACTTAT     360
CGCCACTGGC  AGCAGCCACT  GGTAACAGGA  TTAGCAGAGC     400
GAGGTATGTA  GGCGGTGCTA  CAGAGTTCTT  GAAGTGGTGG     440
CCTAACTACG  GCTACACTAG  AAGGACAGTA  TTTGGTATCT     480
GCGCTCTGCT  GAAGCCAGTT  ACCTTCGGAA  AAAGAGTTGG     520
TAGCTCTTGA  TCCGGCAAAC  AAACCACCGC  TGGTAGCGGT     560
GGTTTTTTTG  TTTGCAAGCA  GCAGATTACG  CGCAGAAAAA     600
AAGGATCT                                           608
```

(2)   INFORMATION FOR SEQ ID NO:27:

        (i)   SEQUENCE CHARACTERISTICS:
                (A)   LENGTH: 1547 base pairs
                (B)   TYPE: nucleic acid
                (C)   STRANDEDNESS: single
                (D)   TOPOLOGY: unknown

        (ii)   MOLECULE TYPE: cDNA

        (iii)   HYPOTHETICAL: No

        (iv)   ANTI-SENSE: No

        (xi)   SEQUENCE DESCRIPTION:SEQ ID NO:27:

```
GGTACCTGCC  ACCATGGCGC  GGATTCTTTA  TCACTGATAA      40
GTTGGTGGAC  ATATTATGTT  TATCAGTGAT  AAAGTGTCAA      80
GCATGACAAA  GTTGCAGCCG  AATACAGTGA  TCCGTGCCGG     120
CCCTGGACTG  TTGAACGAGG  TCGGCGTAGA  CGGTCTGACG     160
ACACGCAAAC  TGGCGGAACG  GTTGGGGGTG  CAGCAGCCGG     200
CGCTTTACTG  GCACTTCAGG  AACAAGCGGG  CGCCTTAAGG     240
GCCATATGGT  GAGTGGATGC  CTTGACCCCA  GGCGGGGATG     280
GGGGAGACCT  GTAGTCAGAG  CCCCCGGGCA  GCACAGGCCA     320
ATGCCCGTCC  TTCCCCTGCA  GGATGAGTAG  TGAGTGCCTC     360
TCCTGGCCCT  GGAAGTTGCC  ACTCCAGTGC  CCACCAGCCT     400
TGTCCTAATA  AAATTAAGTT  GCATCATTTT  GTCTGACTAG     440
GTGTCCTCTA  TAATATTATA  AGCTTGATAT  CGAATTCTTT     480
CGGACTTTTG  AAAGTGATGG  TGGTGGGGGA  AGGATTCGAA     520
CCTTCGAAGT  CGATGACGGC  AGATTTAGAG  TCTGCTCCCT     560
TTGGCCGCTC  GGGAACCCCA  CCACGGGTAA  TGCTTTTACT     600
GGCCTGCTCC  CTTATCGGGA  AGCGGGGCGC  ATCATATCAA     640
ATGACGCGCC  GCTGTAAAGT  GTTACGTTGA  GAAAGAATTC     680
CTGCAGCCCG  CCGCGTTGCT  GGCGTTTTTC  CATAGGCTCC     720
```

```
GCCCCCCTGA CGAGCATCAC AAAAATCGAC GCTCAAGTCA        760
GAGGTGGCGA AACCCGACAG GACTATAAAG ATACCAGGCG        800
TTTCCCCCTG GAAGCTCCCT CGTGCGCTCT CCTGTTCCGA        840
CCCTGCCGCT TACCGGATAC CTGTCCGCCT TTCTCCCTTC        880
GGGAAGCGTG GCGCTTTCTC AATGCTCACG CTGTAGGTAT        920
CTCAGTTCGG TGTAGGTCGT TCGCTCCAAG CTGGGCTGTG        960
TGCACGAACC CCCCGTTCAG CCCGACCGCT GCGCCTTATC       1000
CGGTAACTAT CGTCTTGAGT CCAACCCGGT AAGACACGAC       1040
TTATCGCCAC TGGCAGCAGC CACTGGTAAC AGGATTAGCA       1080
GAGCGAGGTA TGTAGGCGGT GCTACAGAGT TCTTGAAGTG       1120
GTGGCCTAAC TACGGCTACA CTAGAAGGAC AGTATTTGGT       1160
ATCTGCGCTC TGCTGAAGCC AGTTACCTTC GGAAAAAGAG       1200
TTGGTAGCTC TTGATCCGGC AAACAAACCA CCGCTGGTAG       1240
CGGTGGTTTT TTTGTTTGCA AGCAGCAGAT TACGCGCAGA       1280
AAAAAAGGAT CTGGGGGATC CGGAGAGCTC ACTCTAGATG       1320
AGAGAGCAGT GAGGGAGAGA CAGAGACTCG AATTTCCGGA       1360
GCTATTTCAG TTTTCTTTTC CGTTTTGTGC AATTTCACTT       1400
ATGATACCGG CCAATGCTTG GTTGCTATTT TGGAAACTCC       1440
CCTTAGGGGA TGCCCCTCAA CTGGCCCTAT AAAGGGCCAG       1480
CCTGAGCTGC AGAGGATTCC TGCAGAGGAT CAAGACAGCA       1520
CGTGGACCTC GCACAGCCTC TCCCACA                     1547
```

(2)   INFORMATION FOR SEQ ID NO:28:

    (i)   SEQUENCE CHARACTERISTICS:
            (A)   LENGTH: 1807 base pairs
            (B)   TYPE: nucleic acid
            (C)   STRANDEDNESS: single
            (D)   TOPOLOGY: unknown

    (ii)   MOLECULE TYPE: cDNA

    (iii)   HYPOTHETICAL: No

    (iv)   ANTI-SENSE: No

    (xi)   SEQUENCE DESCRIPTION:SEQ ID NO:28:

```
GGTACCTGCC ACCATGGCGC GGATTCTTTA TCACTGATAA         40
GTTGGTGGAC ATATTATGTT TATCAGTGAT AAAGTGTCAA         80
GCATGACAAA GTTGCAGCCG AATACAGTGA TCCGTGCCGG        120
CCCTGGACTG TTGAACGAGG TCGGCGTAGA CGGTCTGACG        160
ACACGCAAAC TGGCGGAACG GTTGGGGGTG CAGCAGCCGG        200
CGCTTTACTG GCACTTCAGG AACAAGCGGG CGCCTTAAGG        240
GCCATATGGT GAGTGGATGC CTTGACCCCA GGCGGGGATG        280
GGGGAGACCT GTAGTCAGAG CCCCCGGGCA GCACAGGCCA        320
ATGCCCGTCC TTCCCCTGCA GGATGAGTAG TGAGTGCCTC        360
TCCTGGCCCT GGAAGTTGCC ACTCCAGTGC CCACCAGCCT        400
TGTCCTAATA AAATTAAGTT GCATCATTTT GTCTGACTAG        440
GTGTCCTCTA TAATATTATA AGCTTGATAT CGAATTCTTT        480
CGGACTTTTG AAAGTGATGG TGGTGGGGGA AGGATTCGAA        520
CCTTCGAAGT CGATGACGGC AGATTTAGAG TCTGCTCCCT        560
TTGGCCGCTC GGGAACCCCA CCACGGGTAA TGCTTTTACT        600
GGCCTGCTCC CTTATCGGGA AGCGGGGCGC ATCATATCAA        640
ATGACGCGCC GCTGTAAAGT GTTACGTTGA GAAAGAATTC        680
```

```
CTGCAGCCCG CCGCGTTGCT GGCGTTTTTC CATAGGCTCC          720
GCCCCCCTGA CGAGCATCAC AAAAATCGAC GCTCAAGTCA          760
GAGGTGGCGA AACCCGACAG GACTATAAAG ATACCAGGCG          800
TTTCCCCCTG GAAGCTCCCT CGTGCGCTCT CCTGTTCCGA          840
CCCTGCCGCT TACCGGATAC CTGTCCGCCT TTCTCCCTTC          880
GGGAAGCGTG GCGCTTTCTC AATGCTCACG CTGTAGGTAT          920
CTCAGTTCGG TGTAGGTCGT TCGCTCCAAG CTGGGCTGTG          960
TGCACGAACC CCCCGTTCAG CCCGACCGCT GCGCCTTATC         1000
CGGTAACTAT CGTCTTGAGT CCAACCCGGT AAGACACGAC         1040
TTATCGCCAC TGGCAGCAGC CACTGGTAAC AGGATTAGCA         1080
GAGCGAGGTA TGTAGGCGGT GCTACAGAGT TCTTGAAGTG         1120
GTGGCCTAAC TACGGCTACA CTAGAAGGAC AGTATTTGGT         1160
ATCTGCGCTC TGCTGAAGCC AGTTACCTTC GGAAAAAGAG         1200
TTGGTAGCTC TTGATCCGGC AAACAAACCA CCGCTGGTAG         1240
CGGTGGTTTT TTTGTTTGCA AGCAGCAGAT TACGCGCAGA         1280
AAAAAAGGAT CTGGGGGATC CGGAGAGCTC CCAACGCGTT         1320
GGATGCATGG ATGAGGGAAA GGAGGTAAGA TCTGTAATGA         1360
ATAAGCAGGA ACTTTGAAGA CTCAGTGACT CAGTGAGTAA         1400
TAAAGACTCA GTGACTTCTG ATCCTGTCCT AACTGCCACT         1440
CCTTGTTGTC CCAAGAAAGC GGCTTCCTGC TCTCTGAGGA         1480
GGACCCCTTC CCTGGAAGGT AAAACTAAGG ATGTCAGCAG         1520
AGAAATTTTT CCACCATTGG TGCTTGGTCA AAGAGGAAAC         1560
TGATGAGCTC ACTCTAGATG AGAGAGCAGT GAGGGAGAGA         1600
CAGAGACTCG AATTTCCGGA GCTATTTCAG TTTTCTTTTC         1640
CGTTTTGTGC AATTTCACTT ATGATACCGG CCAATGCTTG         1680
GTTGCTATTT TGGAAACTCC CCTTAGGGGA TGCCCCTCAA         1720
CTGGCCCTAT AAAGGGCCAG CCTGAGCTGC AGAGGATTCC         1760
TGCAGAGGAT CAAGACAGCA CGTGGACCTC GCACAGCCTC         1800
TCCCACA                                            1807
```

(2) `INFORMATION FOR SEQ ID NO:29:

  (i)   SEQUENCE CHARACTERISTICS:

    (A) LENGTH: 2308 base pairs
    (B) TYPE: nucleic acid

    (C) STRANDEDNESS: single
    (D) TOPOLOGY: unknown

  (ii)   MOLECULE TYPE: cDNA

  (iii)   HYPOTHETICAL: No

  (iv)   ANTI-SENSE: No

  (xi)   SEQUENCE DESCRIPTION:SEQ ID NO:29:

```
GGTACCTGCC ACCATGGCGA AGGGCGAGGA ACTGTTCACT           40
GGCGTGGTCC CAATTCTCGT GGAACTGGAT GGCGATGTGA           80
ATGGGCACAA ATTTTCTGTC AGCGGAGAGG GTGAAGGTGA          120
TGCCACATAC GGAAAGCTCA CCCTGAAATT CATCTGCACC          160
ACTGGAAAGC TCCCTGTGCC ATGGCCAACA CTGGTCACTA          200
CCTTCACCTA TGGCGTGCAG TGCTTTTCCA GATACCCAGA          240
CCATATGAAG CAGCATGACT TTTTCAAGAG CGCCATGCCC          280
```

```
GAGGGCTATG  TGCAGGAGAG  AACCATCTTT  TTCAAAGATG          320
ACGGGAACTA  CAAGACCCGC  GCTGAAGTCA  AGTTCGAAGG          360
TGACACCCTG  GTGAATAGAA  TCGAGTTGAA  GGGCATTGAC          400
TTTAAGGAAG  ATGGAAACAT  TCTCGGCCAC  AAGCTGGAAT          440
ACAACTATAA  CTCCCACAAT  GTGTACATCA  TGGCCGACAA          480
GCAAAAGAAT  GGCATCAAGG  TCAACTTCAA  GATCAGACAC          520
AACATTGAGG  ATGGATCCGT  GCAGCTGGCC  GACCATTATC          560
AACAGAACAC  TCCAATCGGC  GACGGCCCTG  TGCTCCTCCC          600
AGACAACCAT  TACCTGTCCA  CCCAGTCTGC  CCTGTCTAAA          640
GATCCCAACG  AAAAGAGAGA  CCACATGGTC  CTGCTGGAGT          680
TTGTGACCGC  TGCTGGGATC  ACACATGGCA  TGGACGAGCT          720
GTACAAGTGA  GCGCCTTAAG  GGCCATATGG  TGAGTGGATG          760
CCTTGACCCC  AGGCGGGGAT  GGGGGAGACC  TGTAGTCAGA          800
GCCCCGGGC  AGCACAGGCC  AATGCCCGTC  CTTCCCCTGC          840
AGGATGAGTA  GTGAGTGCCT  CTCCTGGCCC  TGGAAGTTGC          880
CACTCCAGTG  CCCACCAGCC  TTGTCCTAAT  AAAATTAAGT          920
TGCATCATTT  TGTCTGACTA  GGTGTCCTCT  ATAATATTAT          960
AAGCTTGATA  TCGAATTCTT  TCGGACTTTT  GAAAGTGATG         1000
GTGGTGGGGG  AAGGATTCGA  ACCTTCGAAG  TCGATGACGG         1040
CAGATTTAGA  GTCTGCTCCC  TTTGGCCGCT  CGGGAACCCC         1080
ACCACGGGTA  ATGCTTTTAC  TGGCCTGCTC  CCTTATCGGG         1120
AAGCGGGGCG  CATCATATCA  AATGACGCGC  CGCTGTAAAG         1160
TGTTACGTTG  AGAAAGAATT  CCTGCAGCCC  GCCGCGTTGC         1200
TGGCGTTTTT  CCATAGGCTC  CGCCCCCCTG  ACGAGCATCA         1240
CAAAAATCGA  CGCTCAAGTC  AGAGGTGGCG  AAACCCGACA         1280
GGACTATAAA  GATACCAGGC  GTTTCCCCCT  GGAAGCTCCC         1320
TCGTGCGCTC  TCCTGTTCCG  ACCCTGCCGC  TTACCGGATA         1360
CCTGTCCGCC  TTTCTCCCTT  CGGGAAGCGT  GGCGCTTTCT         1400
CAATGCTCAC  GCTGTAGGTA  TCTCAGTTCG  GTGTAGGTCG         1440
TTCGCTCCAA  GCTGGGCTGT  GTGCACGAAC  CCCCGTTCA          1480
GCCCGACCGC  TGCGCCTTAT  CCGGTAACTA  TCGTCTTGAG         1520
TCCAACCCGG  TAAGACACGA  CTTATCGCCA  CTGGCAGCAG         1560
CCACTGGTAA  CAGGATTAGC  AGAGCGAGGT  ATGTAGGCGG         1600
TGCTACAGAG  TTCTTGAAGT  GGTGGCCTAA  CTACGGCTAC         1640
ACTAGAAGGA  CAGTATTTGG  TATCTGCGCT  CTGCTGAAGC         1680
CAGTTACCTT  CGGAAAAAGA  GTTGGTAGCT  CTTGATCCGG         1720
CAAACAAACC  ACCGCTGGTA  GCGGTGGTTT  TTTTGTTTGC         1760
AAGCAGCAGA  TTACGCGCAG  AAAAAAAGGA  TCTGGGGGAT         1800
CCGGAGAGCT  CCCAACGCGT  TGGATGCATG  GATGAGGGAA         1840
AGGAGGTAAG  ATCTGTAATG  AATAAGCAGG  AACTTTGAAG         1880
ACTCAGTGAC  TCAGTGAGTA  ATAAAGACTC  AGTGACTTCT         1920
GATCCTGTCC  TAACTGCCAC  TCCTTGTTGT  CCCAAGAAAG         1960
CGGCTTCCTG  CTCTCTGAGG  AGGACCCCTT  CCCTGGAAGG         2000
TAAAACTAAG  GATGTCAGCA  GAGAAATTTT  TCCACCATTG         2040
GTGCTTGGTC  AAAGAGGAAA  CTGATGAGCT  CACTCTAGAT         2080
GAGAGAGCAG  TGAGGGAGAG  ACAGAGACTC  GAATTCCGG          2120
AGCTATTTCA  GTTTTCTTTT  CCGTTTTGTG  CAATTTCACT         2160
TATGATACCG  GCCAATGCTT  GGTTGCTATT  TTGGAAACTC         2200
CCCTTAGGGG  ATGCCCCTCA  ACTGGCCCTA  TAAAGGGCCA         2240
GCCTGAGCTG  CAGAGGATTC  CTGCAGAGGA  TCAAGACAGC         2280
ACGTGGACCT  CGCACAGCCT  CTCCCACA                       2308
```